

# FIGURE 2

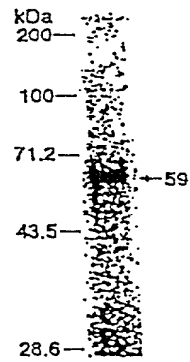


FIGURE 3

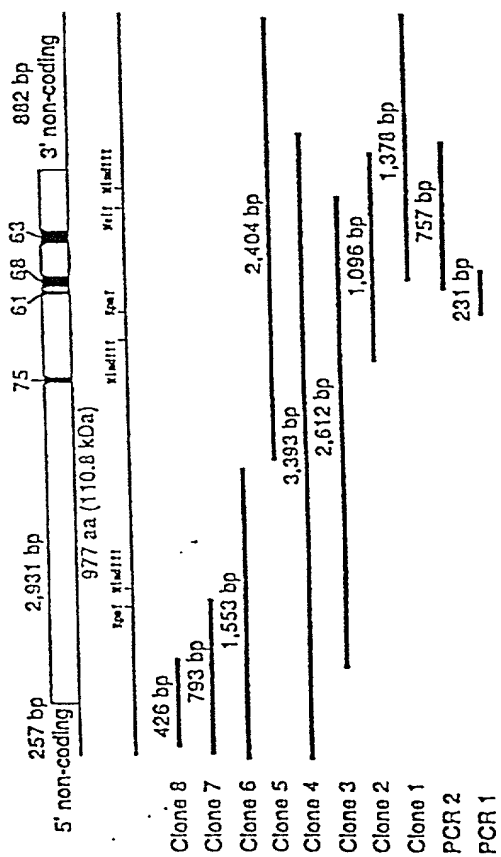
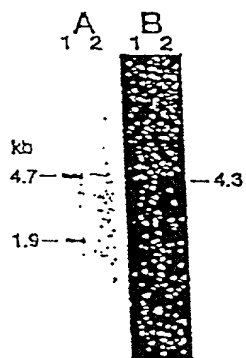


FIGURE 4

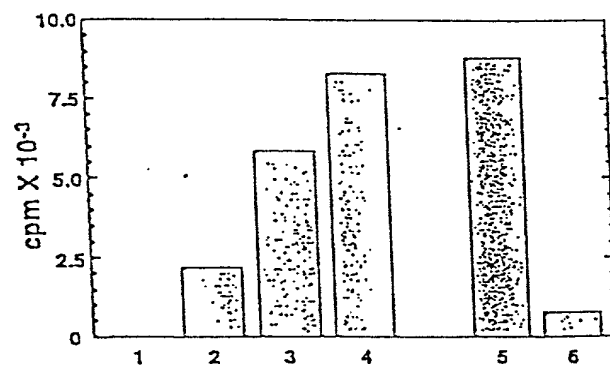


009744-10094  
T0600T-004500

# FIGURE 5

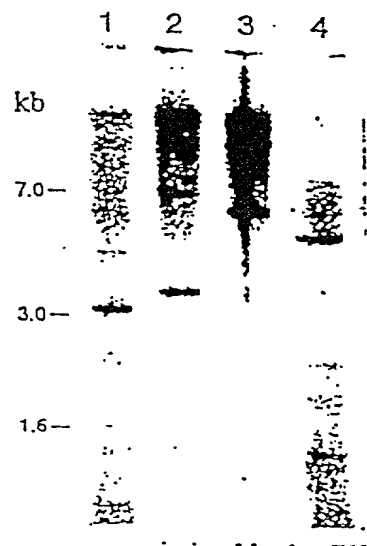
bPARG	(422)	ED...	RRKEQCEMKHQ RTE..	RRIPKYIPPH	SEQ	ID NO:	19
hPARG	(421)	ED...	RRKEQWETKHQ RTE..	RRIPKYVPPH	SEQ	ID NO:	20
mPARG	(413)	ED...	RRKEQCEVRHQ RTE..	RRIPKYIPPN	SEQ	ID NO:	21
CePARG	(29)	HQVPTM	KRRKLTEHGNTTESLL	KEDPEEPS	SEQ	ID NO:	22
hPARG	(205)	EG...	KRKGD.EVDG.	VDEVAKKSKKEKDK	SEQ	ID NO:	23
mPARG	(205)	EG...	KRKGD.EVDG.	TDEVAKKSKRKETDK	SEQ	ID NO:	24
bPARG	(208)	EG...	KRKGD.EVDG.	IDVTKKSKKEKDK	SEQ	ID NO:	25
aPARG	(205)	EG...	KRKGE.EVDG.	NVVAKKSKRKEKEK	SEQ	ID NO:	26
XIPARP	(204)	EG...	KRKAD.EVDG.	HSAATKKIKKEKEK	SEQ	ID NO:	27
DmPARG	(202)	EELPDT	KRAKM.ELSDTNEE	GEKKQR.....	SEQ	ID NO:	28
SpPARG	(205)	EGVSSA	KKAKI.EKIDEEDA	ASTIKELTEKIKK	SEQ	ID NO:	29

**FIGURE 6**



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**FIGURE 7**



**FIGURE 8**

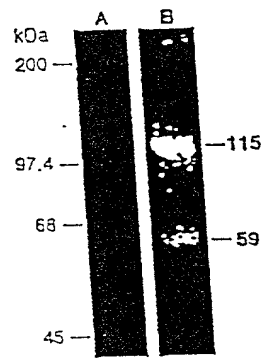
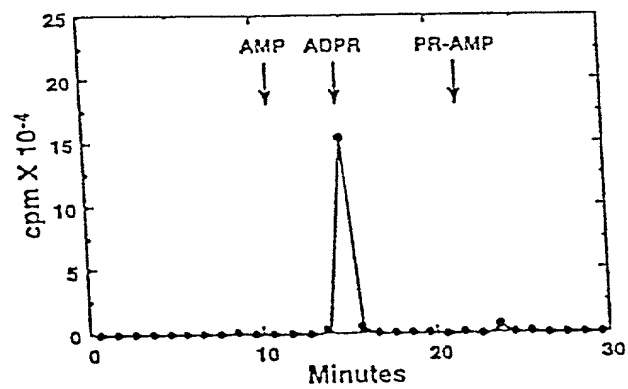




FIGURE 9



1      2      3      4

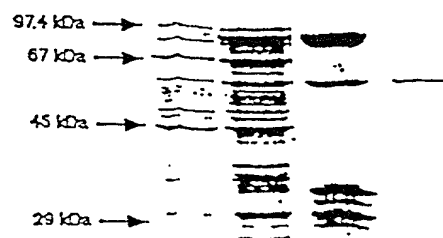


FIGURE 11

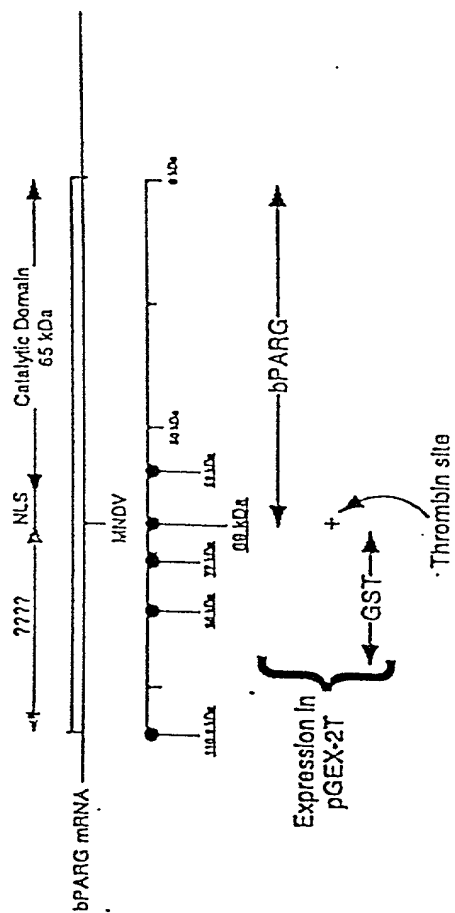


FIGURE 12

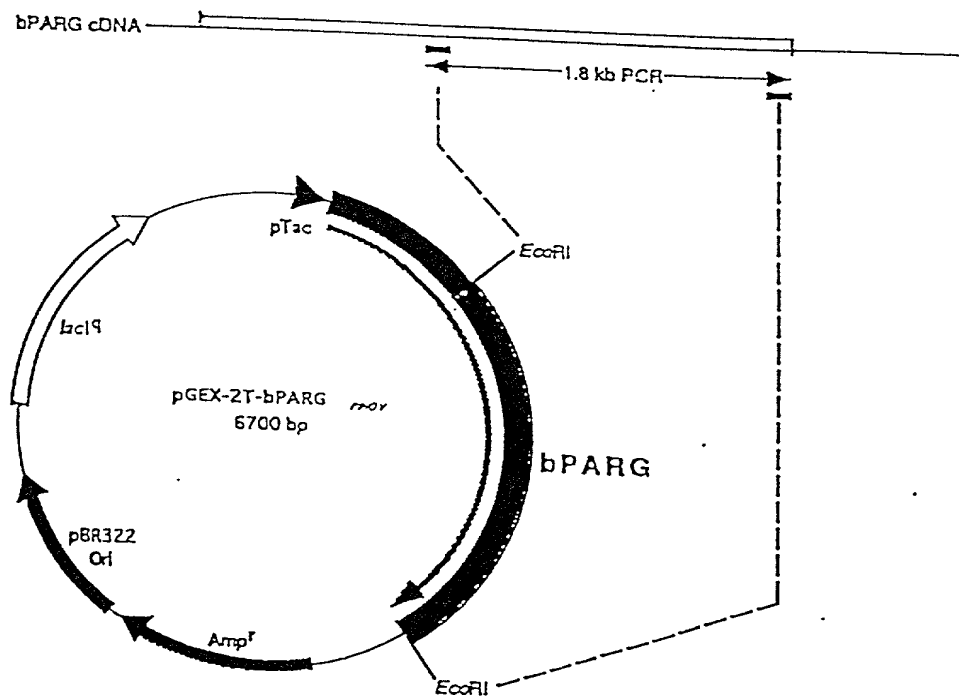
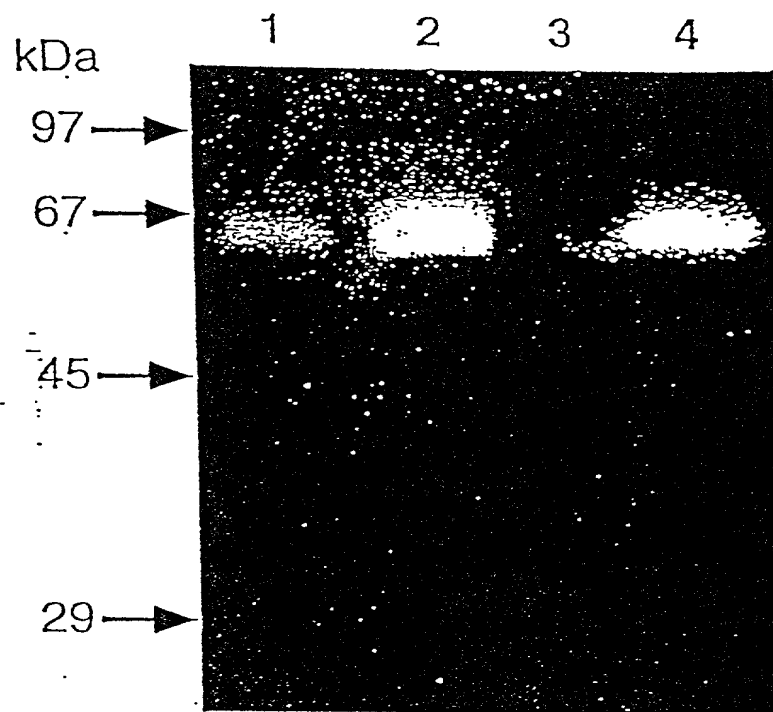
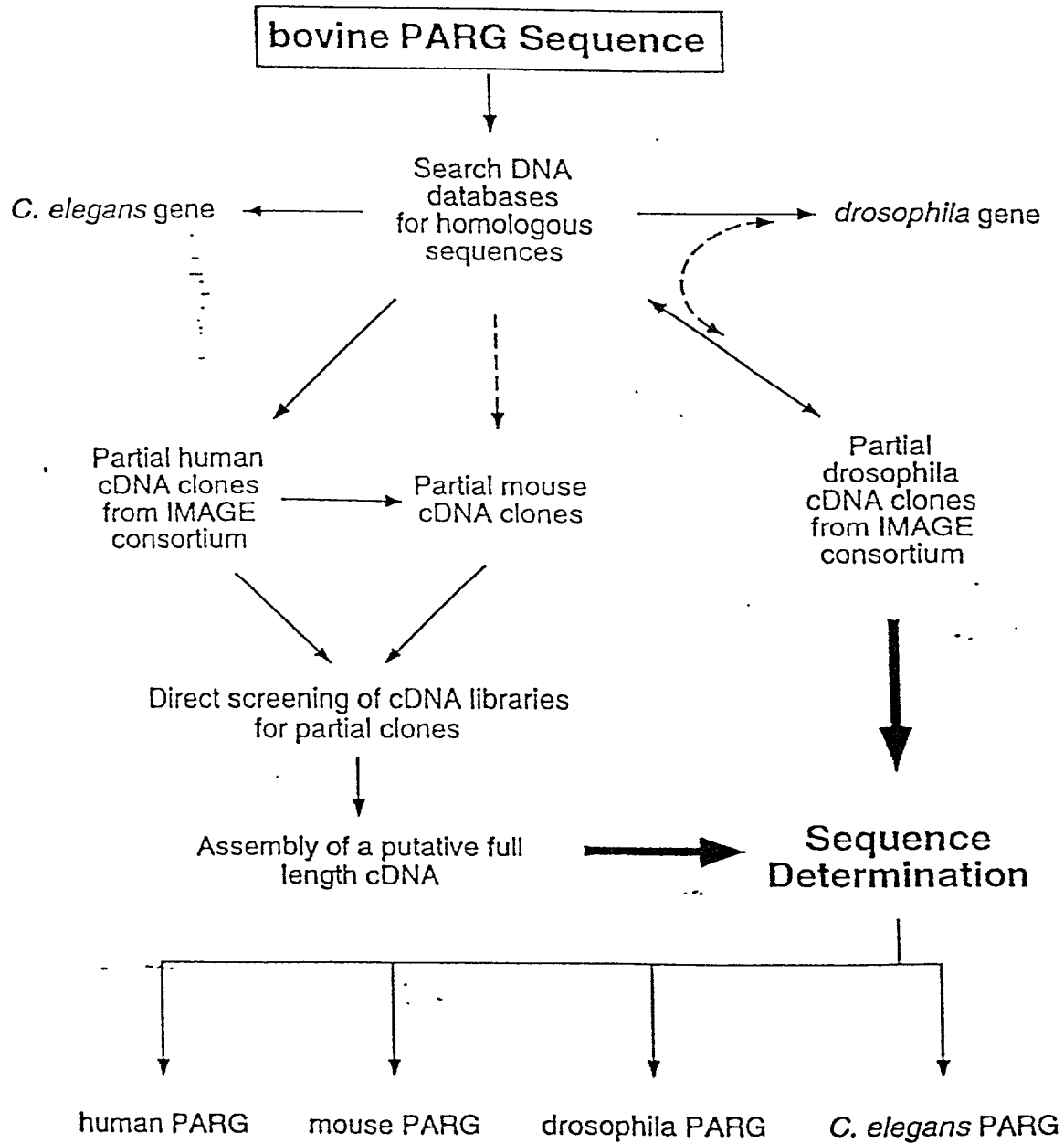


FIGURE 13

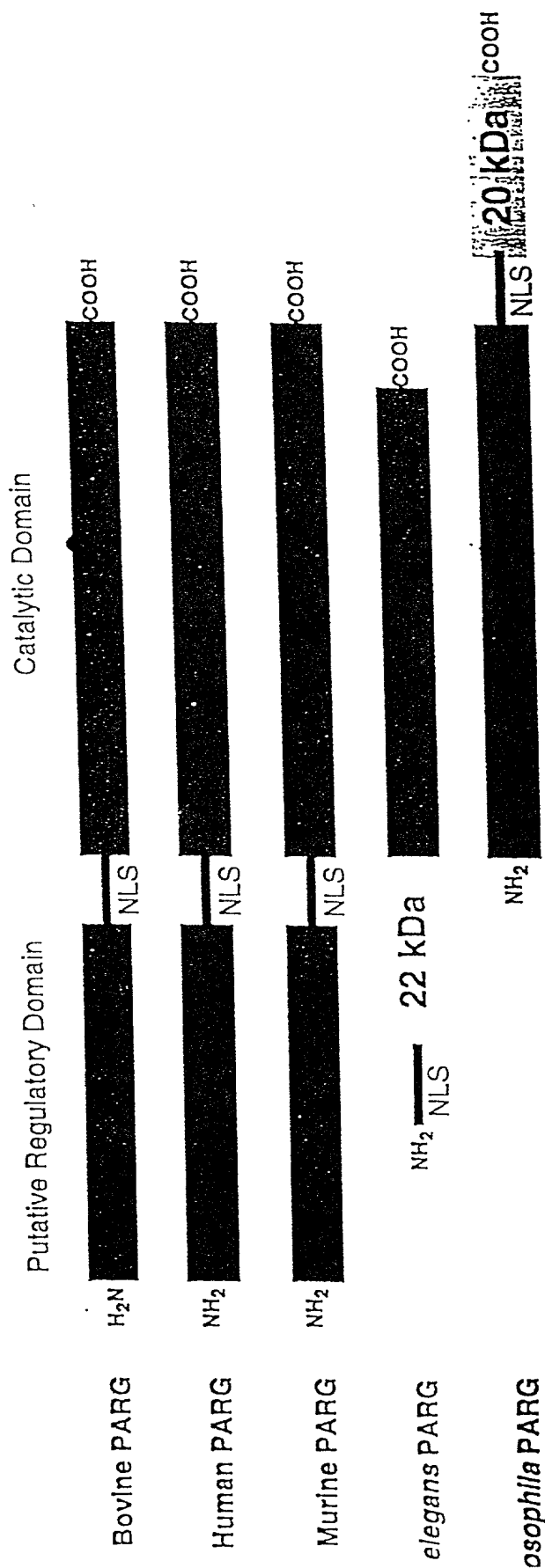


[illegible]

## Strategy to Obtain Homologous PARG Sequences



# Domain Organization of PARs



# FIGURE 16

## Multiple Alignment of Amino Acid Sequences of PARG from Different Species

```

parg      1 MSAGPGCEPCTKRPRWDAATSPPAASDARSFPGRQRRVLDKSDAPVQFRVPPSSSGCALGRAGQHRGATSLSVFKQKTITSNMMDTKGIKTVESESLHSEK
parg      1 MNAGPGCEPCTKATRWGAATTS.PAASDARSFPGRQRRVLDKSDAPVQFRVPPSSSPACVPGQAGQHRGATSLSVFKQKTITSNMMDTKGIKTARSESLDSK
parg      1 MSAGPGWEPTKA.RWGAAGTSAPTASDSRSFPGRQRRVLDKSDAPVQFRVPPSSSPACVSGRAGPHRGATSFVFKQKTITTNMMDTKGPKTAESE...SK
parg      1 -----
cparg     1 -----

101 ENNNTREESMMSSVQKDNFYQHNMKELENVSQLGFDKSPVEKGTQILKQHQTAAMCKWQNEGPKSERLLESEPPAVTLVPEQFSNANVDQSSPKDDHSDT
parg      100 ENNNTRIESMMSSVQKDNFYQHNVKLVNVSQLSLDKSLTEKSTQILNQHQTAAMCKWQNEGPKETEQLLESEPPQTVTLVPEQFSNANIDRSPQNDHSDT
parg      97 ENNNTRIDSMSSVQKDNFYPHKVEKLENVQNLNLDKSPTEKSSQILNQQTASVCKWQNEGKHAEQLLASEPPAGTLPKQLSNANIGQSPHTDDHSDT
parg      1 -----
cparg     1 -----MSKKPIELGDPVTQDEKDYDY

201 NSEESRDNQQLTHVKL...ANAKQTMEDDEQGREARSHQKCGKACHPAEACAGCQQEETDVVSESPLSDTGSEDVGTGLKNANLRNQESSLGNSPPFPEK
parg      200 DSEENRDNQQLTTVKL...ANAKQTEDEHAREAKSHQKCSKSCHPGEDCASCQQDEIDVVPKSPLSDVGSESDVGTGSKNDNKLIRQESSCLGNSPPFPEK
parg      197 DHEEDRDNQQLTPIKL...ANTKPTVGDGQ...ARSNCKCSGSRQSVKDCCTGCGQREVDVLPESPLSDVGAEDIGTGPKNDNKLGTQESSLGDSPPFPEK
parg      1 -----
cparg     23 VGVGFAHQVPTMKRRRLTEHGNTTESKEDPEEPKSRDVVSSQSSDESQEDSAENPEIAKEVSENCENLTETLKISNIESLDNVTERSEHTLDN...HK

298 ESEPESPMDVDNKNKSCQDSEADEETSPGFDE.QEDSSSAQTANKPSRFQPREADTELKRSSAKGGEIRLHFQFEGGESRAGMN.DVNAKRPGSTSSLN
parg      297 ESEPESPMDVDNKNKSCQDSEADEETSPGFDE.QEDGSSSAQTANKPSRFQPREADTELKRSSAKGGEIRLHFQFEGGESRTGMN.DLNAKLPGNISSLN
parg      291 ESEPESPMDVDNKNKSCQDSEADEETSPGFDE.QEDRSS.QTANKLSSQAREADGDLKRRLYLRGSEVRLHFQFEGGENAGTS.DLNAKPSGNSSSLN
parg      1 -----
cparg     119 STEPMEE.DVNNKSNIDVAINSDEDDDLVLEENNKEMRDGEQVQQLS...QDLFADDQELIETPGIMKDDTTQLDITDSQVETAQKMEMIEETADSTFVG

396 VECRNSKQHGKRDSDKITDHFMRVPAEDKRKEQCEMKHQRTERKIPKIIYPHLSFDKWLGTPIEEM...RMMPRCGIRLPLLRPSANHTVTIRVDLLRIG
parg      395 VECRNSKQHGKRDSDKITDHLMLPKAEDRRKEQWETKHQRTERKIPKIIYPHLSFDKWLGTPIEEM...RMMPRCGIRLPLLRPSANHTVTIRVDLLRAG
parg      387 VECRNSKQHGKRDSDKITDHFMRVPAEDKRKEQCEMKHQRTERKIPKIIYPHLSFDKWLGTPIEEM...RMMPRCGIRLPLLRPSANHTVTIRVDLLRAG
parg      32 ....TNRLGK...ALCLNCARMSKSPDGGISEIE.....TEEE.PENLANSL...DDSWRGVSMIAHRNQPFLEENLPVVTAGNLHRVMYQLPIRET.
cparg     216 EDSKATKTVRTSSSS...LSTVSTCEAPAKGRARMYQKELEKHVIAFTEGNLT...LQPDNLKVDPRNIRY.CTIPNFPASQG...KLRED.NRYG

494 EVFK.PFPPTHFKDLWDNKHVKMPCSEQNLYPVEDENGE.RAAGSRWELIQTALLNRLTRPQNLKDAILKYNVAYSKKWDFLTALIDFWDKVLSEEAQHLI
parg      493 EVFK.PFPPTHFKDLWDNKHVKMPCSEQNLYPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKWDFLTALIDFWDKVLSEEAQHLI
parg      485 EVFK.PFPPTHFKDLWDNKHVKMPCSEQNLYPVEDENGE.RTAGSRWELIQTALLNKFTRPQNLKDAILKYNVAYSKKWDFLTALIDFWDKVLSEEAQHLI
parg      115 .PFR.PIKSPGK...WDEHVRVLPAPESKIPRENPDGS.TTIDFRMEMIERALLQPIKTCBELQAAIISYNTTYRDQWHFALHQLLDEELDESETRVVF
cparg     303 .PKIVLPQRWRE.FDSRGR...RDSYFYFKRLDGLKCYKKTGYFMFVGLLH.....NMWE..FDPDITIK...LPAL.EMYIKKMSSELVGRSEV

592 QSILPDWVKIALCLPNICTQPIPLLKQKMHNSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFNRLFEGRSSRKPEKLKTLFCIFRRV..T
parg      591 QSILPDWVKIALCLPNICTQPIPLLKQKMHNSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFNRLFEGRSSRKPEKLKTLFCIFRRV..T
parg      583 QSILPDWVKIALCLPNICTQPIPLLKQKMHNSITMSQEQIASLLANAFFCTFPRRNA.KMKSEYSSYPDINFNRLFEGRSSRKPEKLKTLFCIFRRV..T
parg      210 EDLLPRIIRIALRLPDLIQSPVPLLKHKHNASLSLQQQISCLLANAFCTFPRRMTLRKSEYSTFPDINFNRLFEGRSSRKPEKLKTLFCIFRRV..T
cparg     384 LEKFAVRVARIAKTAEDILPERIYRLVGDVE.SATLSHKQCAALVAKMFFA.....RPDSFSS.....PCRILSSDKSICVEKLFKLTFTIF.....

689 EKK...PTGLVTFTRQS.L.ED.F.PEWERCEKLL..TRLHVTIEGTIEGNGQGMQLQVDFAANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDDH
parg      688 EKK...PTGLVTFTRQS.L.ED.F.PEWERCEKPL..TRLHVTIEGTIEGNGQGMQLQVDFAANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDDH
parg      680 EKK...PTGLVTFTRQS.L.ED.F.PEWERCEKPL..TRLHVTIEGTIEGNGRGMQLQVDFAANRFVGGGVTSAGLVQEEIRFLINPELIVSRLFTFVLDDH
parg      310 ERDASNVPFGVVTFRVRSGLPEH.L.IDWSQSAAPLGDPVPLHVDAGTIEDEIGLQVDFAANKYLGGGVLSHGCVQEEIRFVICPELLVKGFLTECLRP
cparg     463 DKMSMDPPDGAVSF.RLTMDKDTFNEEM.KDKKLSRLPEVEFFDEMLIEDTAL.CTQVDFANEHLGGGVLSHGCVQEEIRFLMCPMMVMVGLLCKMKMQ

779 NECLITGTGEYSEITGYAETIRWA....RSHEDRSE.RDDWQRCTEIVAIIDALHFR.RYLD...QFVPEKIRRELNKATCGFLRPGVSSENLSAVA
parg      778 NECLITGTGEYSEITGYAETIRWS....RSHEDGSE.RDDCERRCTEIVAIIDALHFR.RYLD...QFVPEKMRRELNKATCGFLRPGVSSENLSAVA
parg      770 NECLITGTGEYSEITGYAETIRWA....RSHEDGSE.RDDWQRCTEIVAIIDALHFR.RYLD...QFVPEKVRRELNKATCGFLRPGVSSENLSAVA
parg      408 FEALVMLGAERISNITGIAGSFWS....GNFEDSTP.RDSSGRRTAIVAIIDALHFA.QSHH...QYREDLMERELNKATIGFVHWHVTFP..PGVA
cparg     560 LEAISIVGAIYFSSITGYHTLKWAEQLPNHSRQNTNEFRDRFGRLVETIADAILFKGSKLDCQTEQLNKANIIREMKKASIGFMSQGPFTNIP.IV

868 TGNWCGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELMRDIISMHTFLTERKLTVGE.VIKLLLRYYNEECRNCSTPGP.....DIKLIFFIYHA
parg      867 TGNWCGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELMRDIISMHTFLTERKLTVGD.VIKLLLRYYNEECRNCSTPGP.....DIKLIFFIYHA
parg      859 TGNWCGAFGGDARLKALIQILAAAAAERDVVIFTFGDSELMRDIISMHTFLTERKLDVGG.VIKLLLRYYNEECRNCSTPGP.....DIKLIFFIYHA
parg      495 TGNWCGAFGGDSLKALLQLMVCAQLGRPLAYITFGNVSEFRDDFHEMWLLFRNDGTTVQQ.LWS.ILSYSRLIKEKSSKEPRENKASKKKLYDFI...
cparg     659 TGNWCGAFNGDKPLKFIQVIAAGVADRPLHFCSPGEPLEAAKCKKIIERMKQKDVTLGKSCFSIFS-----

961 VESCTQTNTNPGQRTIGA-----
parg      960 VESCAETADHSGQRTGT-----
parg      952 VESSAETTDMPGQKAGT-----
parg      590 KEELKKVRDVPGEASAEAGSSRVAGLGEGKSETSAKSSPELNKQPARPQITITQQSTDLLPAQLSQDNSNSSEDQALLMLSDDEANAMMEASLEAKS
cparg     727 -----

978 -----
parg      977 -----
parg      969 -----
parg      690 SVEISNSSSTTSSTATKSMGSGGRQLSLLMLDTHYEKGSASKRPRKSPNCSKAEGSAKSKEIDVTDKDEKDDIVD
cparg     727 -----

```



FIGURE 17

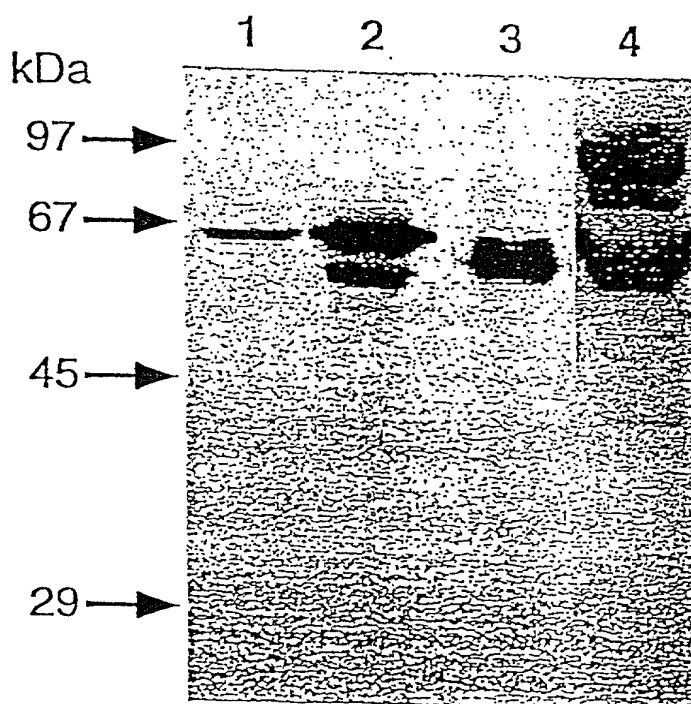


FIGURE 18

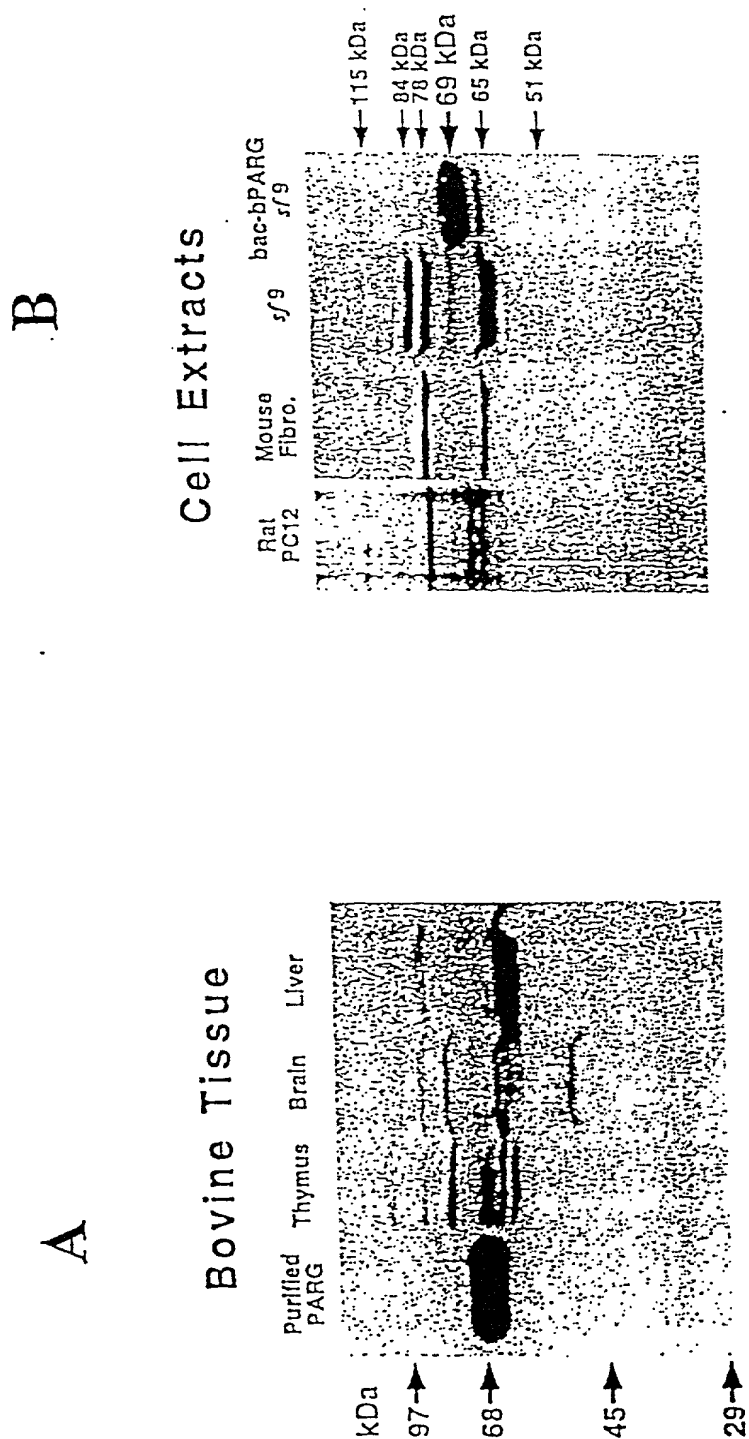


FIGURE 19

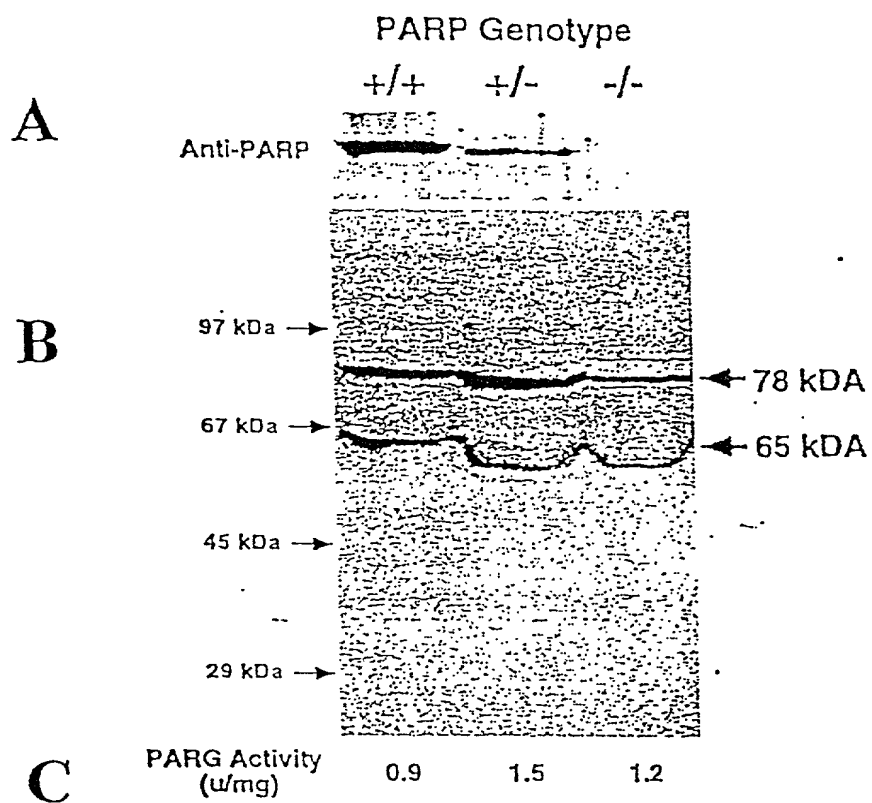


FIGURE 20

Genomic cloning of the PARG gene

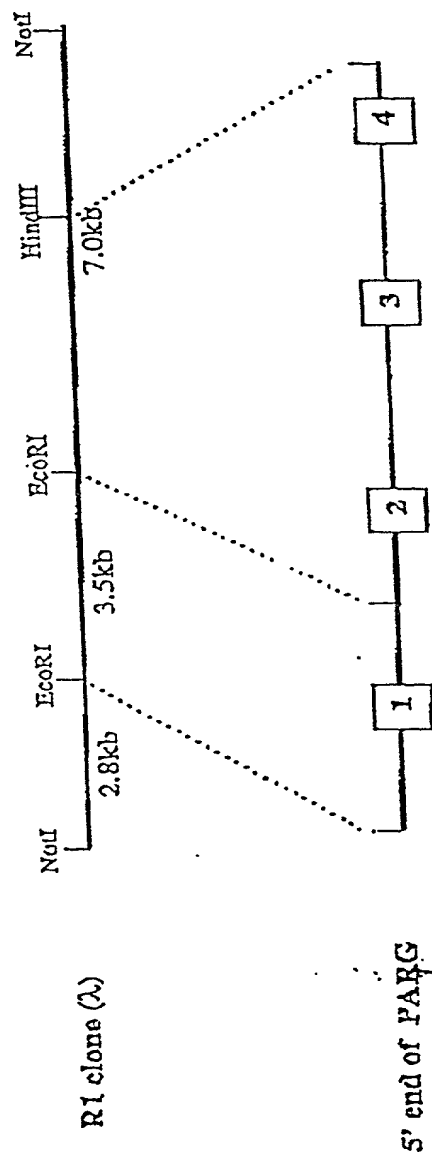


FIGURE 21  
FOCUS OF THE 2550

